REMARKS

A. Status of the Claims

Claims 38 and 41-59 were pending in the case at the time of the Official Action, dated May 17, 2004. All claims stand rejected. Claims 38 and 43-59 stand rejected under 35 U.S.C. § 112, first paragraph. Claims 47-53 stand rejected under 35 U.S.C. § 112, second paragraph. Finally, claims 47-53 stand rejected under 35 U.S.C. § 102(e) as being unpatentable over Fodor *et al.* (U.S. Patent No. 6,582,908).

B. Summary of Examiner Interview on September 14, 2004

On September 14, 2004, the Examiner graciously granted a brief interview with Margaret Sampson to discuss the present application. During the interview, Applicant proposed amending claims 38 as set forth herein. The Examiner agreed to review the amendments, and consider whether the claim is now in condition for allowance. The Examiner also indicated that deleting the term "about" from claim 47, which has been done, would overcome the indefiniteness arguments presented in the last Office Action. Finally, the Examiner indicated that the rejection of claim 54, which is claim 41 rewritten in an independent form and has been indicated by the Examiner as allowable subject matter, is allowable if Applicant makes clear that the claim is directed to an isolated nucleic acid molecule or the complete complement thereof. Applicant has accordingly amended claim 54.

C. Rejections Based on 35 U.S.C. § 112, First Paragraph, are Overcome

Claims 38 and 43-53 stand rejected under 35 U.S.C. § 112, first paragraph, "as containing subject matter which was not described in the specification in such a way as to reasonably convey to

one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention."

1. Independent Claim 38 and Its Dependent Claims 41-46

Claims 38 was rejected under 35 U.S.C. § 112, first paragraph, because "claim 38 permits conservative, but undisclosed, amino acid substitutions, which would necessarily result in undisclosed nucleic acid variation."

Applicant has amended claim 38 to more clearly set forth the scope of the claim, including "the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (Federal Register: December 21, 1999, Vol. 64, No. 244). These common attributes of the claimed nucleic acid molecules and conservative amino acid variants thereof include both: (1) a feature that must be present in the claimed molecule, *i.e.*, that the claimed molecule encode an amino acid sequence in which the binding interaction with CD2 is maintained as compared to the wild-type CD2BP1 protein (which is named CD2 binding protein 1, see paragraph [0094] of the specification); and (2) a feature that must be absent from the claimed molecule, *i.e.*, that the claimed molecule encode an amino acid sequence in which the binding interaction with PTP PEST (protein tyrosine phosphatase, proline-glutamate-serine-threonine rich region) is disrupted as compared to the wild-type CD2BP1 protein. A person of skill in the art clearly would understand an isolated nucleic acid molecule which encodes an amino acid sequence comprising the sequence of SEQ ID NOS:20 or 22, or conservative amino acid variants thereof. Further, the yeast-two hybrid assays set forth in the specification can be used to routinely test whether the amino acid sequence encoded by the nucleic acid molecule has the common attributes set forth in claim 38. As such, and as taught by the specification, Applicant clearly possessed all members of the claimed genus at the

time this application was filed. Claim 38 therefore complies with the written description requirement.

To begin, Applicant respectfully submits that the specification in paragraph 32, beginning on page 12, clearly describes conservative amino acid variants of both SEQ ID NO:20 and SEQ ID NO:22. The described conservative amino acid variants are well understood by one of ordinary skill in the art. Therefore, one of skill in the art can visualize and identify all potential sequences that fall within the scope of claim 38. Applicant nevertheless acknowledges the Examiner's argument that although one of skill in the art understands what amino acids are conservative variants of other amino acids, and that one of skill in the art could easily substitute conservative amino acids in the claimed sequences, one can envision substitutions to the point that the nucleic acid molecule would share zero homology with SEQ ID NOS:20 and 22. Applicant also acknowledges the Examiner's position that in order to meet the written description requirement, claim 38 must set forth common elements or attributes of the claimed sequences, which Applicant was in possession of at the time the application was filed. Applicant has amended claim 38 to set forth these common elements or attributes of the genus of claimed nucleic acid molecules, such that the claim clearly meets the written description requirement.

As set forth in Example 3 of the specification beginning on page 43 at paragraph [00108], a yeast two hybrid system was used to analyze the binding interactions of amino acid sequences encoded by SEQ ID NOS:20 and 22 (A230T and E250Q mutant CD2BP1 proteins, respectively). These experiments demonstrated severely reduced binding between PTP PEST and both the E250Q and A230T mutant CD2BP1 proteins as compared to the wild type CD2BP1 amino acid sequence encoded by the nucleic acid sequence molecule SEQ ID NO:18. Despite this reduced binding interaction with PTP PEST, the mutant proteins maintained binding interactions with CD2 as

compared to the wild type CD2BP1 protein (see paragraphs [00108]-[00110]). Applicant proposed that the two identified mutations in the CD2BP1 gene disclosed in the present application disrupt a biologically critical binding interaction with PTP PEST, which causes PAPA syndrome (see paragraph [00111] of the specification).

Thus, common characteristics or attributes of the mutant proteins disclosed, as well as all claimed conservative amino acid variants thereof, is that they maintain binding interactions with CD2 but binding interactions with PTP PEST are significantly disrupted as compared to the wild-type CD2BP1 protein. In addition, one of skill in the art can use the yeast two-hybrid system set forth in the specification to routinely test whether a conservative variant of the isolated nucleic acid molecules falls within the scope of claim 38. While this will require experimentation, this experimentation is routine, and not undue. Thus, one of skill in the art would clearly understand that Applicant possessed the full scope of this claim at the time the application was filed.

Including these common characteristics or attributes of the sequences that fall within the scope of claim 38 clearly meets the written description requirement, as set forth in the Revised Interim Guidelines on the written description requirement proposed by the PTO in 64 Fed. Reg. 71427 (Dec. 21, 1999). Under the Revised Interim Guidelines, an inventor can demonstrate possession of an invention by sufficiently describing relevant identifying characteristics of the invention, including "functional characteristics when coupled with a known or disclosed correlation between function and structure. *Id.* at 71435. Clearly the functional characteristics set forth in claim 38, when combined with known sequences, and known conservative amino acid variants thereof, meet the written description requirement as understood by the PTO. Therefore, Applicant respectfully requests withdrawal of this rejection.

2. Independent Claim 47 and Its Dependent Claims 48-53

Claims 47-52 were rejected under 35 U.S.C. § 112, first paragraph, because "these claims encompass the full length gene with conservative substitutions as above since the claims are of the open 'comprising' format," which "negates [a size for the oligonucleotide] as an upper bound to the nucleic acid molecule."

Initially, Applicant would like to clarify the subject matter of claim 47, since it does not as the Examiner suggests claim a full length gene with conservative amino acid substitutions. Rather, claim 47 is directed to an isolated nucleic acid molecule that comprises at least 20 contiguous nucleotides of SEQ ID NO:18 (the wild-type CD2BP1 sequence) with a specifically mutated nucleotide at nucleotide 688 or nucleotide 748 of SEQ ID NO:18, or at both positions. No where does the claim mention conservative amino acid variants thereof. Those of skill in the art will clearly understand whether an isolated nucleic acid sequence falls within the scope of claim 47 because they will be able to see that the isolated nucleic acid sequence has at least 20 contiguous nucleotides that meet one of the three elements set forth in claim 47.

It is routine to claim inventions with comprising language such that the invention is defined by what it must have, not by all the possible things that may also be present in, for example, a claimed composition. For example, if a claim is directed to "An invention comprising elements A, B, and C," this claim will cover the same invention with additional elements. Thus, if another entity begins to sell a product with elements A, B, C, and D, this product will be held to infringe the above claim. There is no requirement to define all potential elements that fall under D to meet the written description requirement, and to do so would be nearly impossible. Likewise, claim 47 clearly sets forth the population of isolated nucleic acid sequences that will fall within its scope, *i.e.*, those that comprise at least 20 contiguous nucleotides of SEQ ID NO:18 (the wild-type CD2BP1 sequence)

with a specifically mutated nucleotide at nucleotide 688 or nucleotide 748 of SEQ ID NO:18, or at both positions. SEQ ID NO:18 is clearly defined in the specification, and determining when an A is located at position 688 or a C is located at position of 748 of SEQ ID NO:18 is clearly within the scope of one of skill in the art. Therefore, the Examiner's suggestion that this genus is not defined and does not have written description is not correct. Accordingly, Applicant respectfully requests withdrawal of this rejection.

With respect to claim 53, it was previously revised to clarify that the oligonucleotides encompassed by this claim are those that hybridize to the nucleic acid molecule of claim 47 but will not substantially hybridize to the corresponding region of the nucleic acid molecule consisting of SEQ ID NO:18. Since a molecule that hybridizes to a nucleic acid molecule of claim 47, but will not hybridize to the corresponding region of the nucleic acid molecule SEQ ID NO:18, will differ by a single nucleotide (at position 688 or 748), this population of nucleotides will actually be a very small genus easily understood by one of skill in the art. Thus, claim 53 is directed to nucleic acid molecules that can detect single nucleotide polymorphisms (SNPs). Again, one of skill in the art can use routine experimentation to determine whether a nucleic acid molecule can differentially hybridize to the nucleic acid sequence of claim 47 but not the corresponding region of wild-type SEQ ID NO:18. Therefore, Applicant respectfully requests withdrawal of this rejection.

3. Independent Claim 47 and Its Dependent Claims 48-53

Claims 54-59 were rejected under 35 U.S.C. § 112, first paragraph, because the claims did not require that the sequence be "fully complementary." Claim 54 has been amended to claim the "complete" complement of the claimed nucleic acid molecule, thereby overcoming this rejection.

D. Rejection Based on 35 U.S.C. § 112, Second Paragraph, is Overcome

Claims 47-53 stand rejected under 35 U.S.C. § 112, second paragraph, as being indefinite because of the phrase "at least about 20 contiguous nucleotides."

Applicant respectfully disagrees that the phrase "at least about 20 contiguous nucleotides" in claim 47 is indefinite. Nevertheless, in an effort to facilitate prosecution of the present application, Applicant has amended claim 47 to delete the term "about." Applicant respectfully asserts that the phrase "at least 20 contiguous nucleotides" is not indefinite, and would be well understood by one of skill in the art. Accordingly, Applicant respectfully requests that the Examiner withdraw this rejection. Applicant takes this action merely to allow claim 47 and its dependent claims to progress to issuance, and reserves the right to pursue claims drawn to any canceled subject matter in this or a related patent application.

E. Rejection Based on 35 U.S.C. § 102(e) is Overcome

Claims 47-53 stand rejected under 35 U.S.C. § 102(e) as being anticipated by Fodor because the "phrase 'about' permits some flexibility in the length of the oligonucleotide" and is deemed by the Examiner to "be a broad term which permits the 10-mer nucleic acids of Fodor to apply."

Applicant respectfully disagrees that the phrase "about 20 contiguous nucleotides" in claim 47 is anticipated by Fodor. Nevertheless, as indicated above, in an effort to facilitate prosecution of the present application, Applicant has amended claim 47 to delete the term "about." Since the phrase "at least 20" is a minimum point that cannot include a 10-mer, Fodor does not anticipate claims 47-53. Therefore, Applicant respectfully requests withdrawal of this rejection.

CONCLUSION

It is Applicant's belief that the claims are in condition for allowance. Such favorable action is respectfully requested. If the Examiner has any questions or comments regarding any issue associated with this application, the undersigned representative respectfully requests that the Examiner contact her at 512/542-8569.

Respectfully submitted,

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